



SEQUENCE LISTING

<110> FRENCH, Cynthia K.
YAMAMOTO, Karen K.
EL SHAMI, A. Said

<120> Prostate Cancer-Specific Marker

<130> 107-206-C-D

<140> 09/680,121

<141> 2000-10-04

<150> 60/041,246

<151> 1997-03-07

<150> 60/047,811

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<150> 09/036,315

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<150> 09/535,597

<151> 2000-03-27

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<151> 2000-10-04

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<170> PatentIn Ver. 2.1

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<222> (151)..(1425)

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20

cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 1
74

Met Ala Pro Ile Thr Thr Ser Arg

1

5

gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 2
22

Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
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ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga 2
70

Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
25 30 35 40

aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 3
18

Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
45 50 55

ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 3
66

Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
60 65 70

ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca 4
14

Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
75 80 85

aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat 4
62

Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn
90 95 100

ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat 5
10

Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn
105 110 115 120

gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct	5
58	
Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro	
125 130 135	
gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag	6
06	
Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu	
140 145 150	
aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa	6
54	
Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys	
155 160 165	
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02	
Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp	
170 175 180	
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Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro	
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98	
Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp	
205 210 215	
cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa	8
46	
Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln	
220 225 230	
atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt	8
94	
Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe	
235 240 245	
tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att	9
42	
Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile	
250 255 260	
gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga	9

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90
Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg
265                270                275                280

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Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys
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tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga   1
086
Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg
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cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa   1
134
His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys
                315                320                325

gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat   1
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Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His
                330                335                340

gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt   1
230
Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
345                350                355                360

gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt   1
278
Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
                365                370                375

ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc   1
326
Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
                380                385                390

ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc   1
374
Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
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tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat   1
422

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Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
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Gly
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095

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<211> 425

<212> PRT

<213> Homo sapiens

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<223> product = Repro-PC-1.0

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Phe	Ala	Trp	Ile	Cys	Cys	Gln	Arg	Lys	Ser	Ser	Lys	Ser	Asn	Lys	Thr	35	40	45	
Pro	Pro	Tyr	Lys	Phe	Val	His	Val	Leu	Lys	Gly	Val	Asp	Ile	Tyr	Pro	50	55	60	
Glu	Asn	Leu	Asn	Ser	Lys	Lys	Lys	Phe	Gly	Ala	Asp	Asp	Lys	Asn	Glu	65	70	75	80
Val	Lys	Asn	Lys	Pro	Ala	Val	Pro	Lys	Asn	Ser	Leu	His	Leu	Asp	Leu	85	90	95	
Glu	Lys	Arg	Asp	Leu	Asn	Gly	Asn	Phe	Pro	Lys	Thr	Asn	Leu	Lys	Pro	100	105	110	
Gly	Ser	Pro	Ser	Asp	Leu	Glu	Asn	Ala	Thr	Pro	Lys	Leu	Phe	Leu	Glu	115	120	125	
Gly	Glu	Lys	Glu	Ser	Val	Ser	Pro	Glu	Ser	Leu	Lys	Ser	Ser	Thr	Ser	130	135	140	
Leu	Thr	Ser	Glu	Glu	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Leu	Phe	Phe	Ser	145	150	155	160
Leu	Glu	Tyr	Asn	Phe	Glu	Arg	Lys	Ala	Phe	Val	Val	Asn	Ile	Lys	Glu	165	170	175	
Ala	Arg	Gly	Leu	Pro	Ala	Met	Asp	Glu	Gln	Ser	Met	Thr	Ser	Asp	Pro	180	185	190	
Tyr	Ile	Lys	Met	Thr	Ile	Leu	Pro	Glu	Lys	Lys	His	Lys	Val	Lys	Thr	195	200	205	
Arg	Val	Leu	Arg	Lys	Thr	Leu	Asp	Pro	Ala	Phe	Asp	Glu	Thr	Phe	Thr	210	215	220	
Phe	Tyr	Gly	Ile	Pro	Tyr	Thr	Gln	Ile	Gln	Glu	Leu	Ala	Leu	His	Phe	225	230	235	240


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Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
      245                      250                      255

Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
      260                      265                      270

Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg
      275                      280                      285

Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
      290                      295                      300

Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser
305                      310                      315                      320

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
      325                      330                      335

Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
      340                      345                      350

Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu
      355                      360                      365

Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
      370                      375                      380

Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr
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Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile
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Ala Lys Trp His Val Leu Cys Asp Gly
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<213> rat

<220>

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5

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15

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu

20

25

30

Phe Ala Trp Ile Cys Cys Gln Arg Arg Ser Ala Lys Ser Asn Lys Thr

35

40

45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro

50

55

60

Glu Asn Leu Ser Ser Lys Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu

65

70

75

80

Ala	Lys	Arg	Lys	Ala	Ala	Leu	Pro	Asn	Leu	Ser	Leu	His	Leu	Asp	Leu	85	90	95
Glu	Lys	Arg	Asp	Leu	Asn	Gly	Asn	Phe	Pro	Lys	Thr	Asn	Pro	Lys	Ala	100	105	110
Gly	Ser	Ser	Ser	Asp	Leu	Glu	Asn	Val	Thr	Pro	Lys	Leu	Phe	Pro	Glu	115	120	125
Thr	Glu	Lys	Glu	Ala	Val	Ser	Pro	Glu	Ser	Leu	Lys	Ser	Ser	Thr	Ser	130	135	140
Leu	Thr	Ser	Glu	Glu	Lys	Gln	Glu	Lys	Leu	Gly	Thr	Leu	Phe	Leu	Ser	145	150	155
Leu	Glu	Tyr	Asn	Phe	Glu	Lys	Lys	Ala	Phe	Val	Val	Asn	Ile	Lys	Glu	165	170	175
Ala	Gln	Gly	Leu	Pro	Ala	Met	Asp	Glu	Gln	Ser	Met	Thr	Ser	Asp	Pro	180	185	190
Tyr	Ile	Lys	Met	Thr	Ile	Leu	Pro	Glu	Lys	Lys	His	Lys	Val	Lys	Thr	195	200	205
Arg	Val	Leu	Arg	Lys	Thr	Leu	Asp	Pro	Val	Phe	Asp	Glu	Thr	Phe	Thr	210	215	220
Phe	Tyr	Gly	Val	Pro	Tyr	Pro	His	Ile	Gln	Glu	Leu	Ser	Leu	His	Phe	225	230	235
Thr	Val	Leu	Ser	Phe	Asp	Arg	Phe	Ser	Arg	Asp	Asp	Val	Ile	Gly	Glu	245	250	255
Val	Leu	Val	Pro	Leu	Ser	Gly	Ile	Glu	Leu	Ser	Asp	Gly	Lys	Met	Leu	260	265	270
Met	Thr	Arg	Glu	Ile	Ile	Lys	Arg	Asn	Ala	Lys	Lys	Ser	Ser	Gly	Arg	275	280	285
Gly	Glu	Leu	Leu	Val	Ser	Leu	Cys	Tyr	Gln	Ser	Thr	Thr	Asn	Thr	Leu	290	295	300
Thr	Val	Val	Val	Leu	Lys	Ala	Arg	His	Leu	Pro	Lys	Ser	Asp	Val	Ser	305	310	315

Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys
 325 330 335
 Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala
 340 345 350
 Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu
 355 360 365
 Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg
 370 375 380
 Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser
 385 390 395 400
 Gly Gly Gly His Trp Lys Glu Ile Cys Asp Phe Pro Arg Arg Gln Ile
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 Ala Lys Trp His Met Leu Cys Asp Gly
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<212> PRT

<213> Homo sapiens

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<223> PKC-C2 internal repeat (amino acid positions
154-271)

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 Arg Ile Tyr Leu Glu Ile Asn Val Lys Glu Asn Leu Leu Thr Val Gln
 20 25 30
 Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser
 35 40 45
 Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser
 50 55 60

Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn
 65 70 75 80
 Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile
 85 90 95
 Leu Ile Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met
 100 105 110
 Gly Ala Leu Ser Phe
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 <213> Homo sapiens

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 <223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino
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 20 25 30
 Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser
 35 40 45
 Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser
 50 55 60
 Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn
 65 70 75 80
 Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser
 85 90 95
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 100 105 110

Ile Gly Gln Leu Val Leu Gly Ala Ala
 115 120

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 <223> synaptotagmin "B" internal repeat (amino acid
 positions 268-383)

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 20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile
 35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile
 50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu
 65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu
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Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val
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Gly Tyr Asn
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<210> 9
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<223> synaptotagmin "A" internal repeat (amino acid positions 134-254)

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Leu	Asp	Tyr	Asp	Phe	Gln	Asn	Asn	Gln	Leu	Leu	Val	Gly	Ile	Ile	Gln
			20					25					30		

Ala	Ala	Glu	Leu	Pro	Ala	Leu	Asp	Met	Gly	Gly	Thr	Ser	Asp	Pro	Tyr
		35					40					45			

Val	Lys	Val	Phe	Leu	Leu	Pro	Asp	Lys	Lys	Lys	Lys	Phe	Glu	Thr	Lys
	50					55					60				

Val	His	Arg	Lys	Thr	Leu	Asn	Pro	Val	Phe	Asn	Glu	Gln	Phe	Thr	Phe
65					70					75					80

Lys	Val	Pro	Tyr	Ser	Glu	Leu	Gly	Gly	Lys	Thr	Leu	Val	Met	Ala	Val
				85					90					95	

Tyr	Asp	Phe	Asp	Arg	Phe	Ser	Lys	His	Asp	Ile	Ile	Gly	Glu	Phe	Lys
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Val	Pro	Met	Asn	Thr	Val	Asp	Phe
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<213> Homo sapiens

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<222> (1)..(113)

<223> Repro=PC-1.0 (PC-20) "A" internal repeat amino acid positions 150-263)

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			20					25					30					
Ala	Met	Asp	Glu	Gln	Ser	Met	Thr	Ser	Asp	Pro	Tyr	Ile	Lys	Met	Thr			
		35					40					45						
Ile	Leu	Pro	Glu	Lys	Lys	His	Lys	Val	Lys	Thr	Arg	Val	Leu	Arg	Lys			
	50					55					60							
Thr	Leu	Asp	Pro	Ala	Phe	Asp	Glu	Thr	Phe	Thr	Phe	Tyr	Gly	Ile	Pro			
	65				70					75					80			
Tyr	Thr	Gln	Ile	Gln	Glu	Leu	Ala	Leu	His	Phe	Thr	Ile	Leu	Ser	Phe			
			85						90					95				
Asp	Arg	Phe	Ser	Arg	Asp	Asp	Ile	Ile	Gly	Glu	Val	Leu	Ile	Pro	Leu			
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Ser

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<212> PRT

<213> Homo sapiens

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<221> Modified-site

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<223> Xaa=Asp, Glu, Ala, Ser or Thr

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<222> 3-8

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<223> Xaa=Any natural or synthetic amino acid

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr

1

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<210> 12

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<212> PRT

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<223> Xaa=Any natural or synthetic amino acid

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Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln
 20 25 30

<210> 22

<211> 34

<212> PRT

<213> Homo sapiens

<400> 22

Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val Leu
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Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys Phe
 20 25 30

Gly Ala

<210> 23

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<212> PRT

<213> Homo sapiens

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Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu Gly
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Glu Lys Glu Ser Val Ser Pro Glu Ser
 20 25

<210> 24

<211> 60

<212> PRT

<213> Homo sapiens

<400> 24

Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr
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Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr
 20 25 30

Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp

35	40	45
Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu		
50	55	60

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Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu Met Asn
1 5 10 15

Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu
20 25 30

Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
35 40 45

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Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu
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Val Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu
20 25 30

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<223> Xaa=Val or Ile

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Ser Asp Pro Tyr Xaa Lys
1 5